

Supplemental Material

Supplemental Material, Table 1. Genes differentially expressed in liver samples of rat offspring exposed perinatally to BDE-47.

Supplemental Material, Figure 1. Schemes of pathways enriched significantly by genes expressed differentially in exposed groups of rats *versus* controls according to Ingenuity Pathway Analysis: LPS/IL-1 Mediated Inhibition of RXR Function; PXR/RXR Activation; Fatty Acid Metabolism; Glycolysis/Gluconeogenesis; Starch and Sucrose Metabolism. The symbols of proteins which genes were over- or down-expressed in G3 appear in red and green, respectively. A red or green circle near the molecule symbol indicates the direction of gene expression change in G2 if different from in G3.

Supplementary file 1. Genes differentially expressed in liver samples of rat offspring exposed perinatally to BDE-47.

Target ID	GenBank accession no.	Definition	Expression fold change (log2)	
			0.002 mg/kg bw	0.2 mg/kg bw
SDS	NM_053962	Serine dehydratase	-0.943	-1.265
SULT1B1	NM_022513.1	Sulfotransferase family, cytosolic, 1B, member 1	0.412	1.164
CYP4A1	NM_175837.1	Cytochrome P450, family 4, subfamily a, polypeptide 1	1.029	1.080
PER2	NM_031678.1	Period homolog 2 (Drosophila)	-1.053	-1.355
LOC499638	XM_574960.1	PREDICTED: similar to LRRGT00057 (LOC499638)	-0.600	-1.418
GSTA2	NM_017013.4	Glutathione S-transferase A2	1.190	1.308
LOC367102	XM_345948.2	PREDICTED: similar to 40S ribosomal protein S9	1.420	2.306
TM7SF2	BC091237	Transmembrane 7 superfamily member 2	1.008	1.000
SLC3A2	NM_019283.1	Solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	1.028	0.633
UGT1A1	NM_012683.2	UDP glucuronosyltransferase 1 family, polypeptide A1	1.071	1.400
DCP1A	XM_341395	DCP1 decapping enzyme homolog A (S. cerevisiae)	-0.578	-1.130
LOC497779	XM_579526.1	PREDICTED: hypothetical gene supported by NM_031736	1.549	-0.089
SULT1C3	NM_031732.1	Sult1c3 sulfotransferase family, cytosolic, 1C, member 3	0.315	1.025
NFIX	XM_001071608.1	Nuclear factor I/X (CCAAT-binding transcription factor)	-0.628	-1.100
LOC306428	XM_224824	PREDICTED: similar to Chain A, T13s Mutant Of Bovine 70 Kilodalton Heat Shock Protein	-0.924	-1.377
CTSC	NM_017097.1	Cathepsin C	0.671	1.059
NNMT	XM_001066533.1	Nicotinamide N-methyltransferase	-0.634	-1.213
RARRES1_PREDICTED	XM_227232.3	PREDICTED: retinoic acid receptor responder (tazarotene induced) 1	0.525	1.045
LOC500525	XM_575886.1	PREDICTED: similar to Cytochrome P450 4A2 precursor (CYP1A2) (Lauric acid omega-hydroxylase) (P450-LA-omega 2) (P450 K-5) (P-450 K-2)	1.281	1.263

LOC361117	XM_341405.2	Similar to Rb1-inducible coiled coil protein 1	-0.703	-1.378
HAO2	NM_032082.1	Hydroxyacid oxidase 2 (long chain)	0.405	1.065
AK3L1	NM_017135	Adenylate kinase 3-like 1	0.466	1.038
LOC498076	XM_573278.1	PREDICTED: similar to RIKEN cDNA 2410116I05	-0.729	-1.244
TUBB2A	XM_574013.2	Tubulin, beta 2a	0.583	1.093
LOC497794	XM_579477.1	PREDICTED: hypothetical gene supported by NM_023103	1.260	1.971
LOC287167	NM_001013853.1	Globin, alpha	-1.137	-0.325
LOC366322	XM_575778.1	PREDICTED: similar to Chain A, Bhmt From Rat Liver	0.940	1.144
CYP2C	NM_019184	Cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase)	0.489	1.054
POR	NM_031576.1	P450 (cytochrome) oxidoreductase	-0.506	-1.393
IGFBP2	NM_013122	Insulin-like growth factor binding protein 2	0.483	1.023
GSTM2	NM_177426.1	Glutathione S-transferase, mu 2	0.748	1.152
G6PC	NM_013098	Glucose-6-phosphatase, catalytic subunit	1.519	1.495
CRP	NM_017096	C-reactive protein, pentraxin-related	1.099	1.263
RGD1560015	XM_574311	Similar to glycoprotein, synaptic 2	0.755	1.011
LOC294046	XM_215267.3	PREDICTED: similar to heat shock protein 8	-0.822	-1.187
RHOA	NM_057132	Ras homolog gene family, member A	0.565	1.221
RGD1565908	XM_226326.3	Similar to L-lactate dehydrogenase A chain (LDH-A) (LDH muscle subunit) (LDH-M)	0.841	1.193
INSIG2	NM_178091	Insulin induced gene 2	1.092	1.552
NPM1	NM_012992	Nucleophosmin (nucleolar phosphoprotein B23, numatrin)	0.892	1.193
CYP7A1	NM_012942.1	Cytochrome P450, family 7, subfamily a, polypeptide 1	0.053	-1.290
LOC360228	NM_001003706	WDNM1 homolog	-0.427	-1.024
LOC498245	XM_573468.1	PREDICTED: similar to LRRGT00176	-0.749	-1.357
USP2	NM_053774.2	Ubiquitin specific peptidase 2	-0.546	-1.231
RGD1564296	XM_577971	PREDICTED: similar to Ac1147	-0.858	-2.489
CYP4A3	NM_175760.2	Cytochrome P450, family 4, subfamily a, polypeptide 3	1.312	1.184
ALDH9A1	NM_022273.2	Aldehyde dehydrogenase 9 family, member A1	0.902	1.107
ACLY	NM_016987	ATP citrate lyase	-0.500	-1.219
SERPINA7	XM_343823.2	Serine (or cysteine) peptidase inhibitor, clade A (alpha-1	0.401	1.355

		antipeptidase, antitrypsin), member 7		
EIF4G2	XM_341907	Eukaryotic translation initiation factor 4, gamma 2	0.815	1.156
CYP2C7	NM_017158.1	Cytochrome P450, family 2, subfamily c, polypeptide 7	1.197	-0.217
LOC292539	XM_214799	Similar to 60S ribosomal protein L17 (L23)	1.776	0.919
LOC500586	XM_575955.1	PREDICTED: similar to LRRGT00057	-0.711	-1.418
A1BG	NM_022258.2	Alpha-1-B glycoprotein	-0.642	-1.077
LOC361417	XM_346974.1	PREDICTED: hypothetical LOC361417	1.021	1.199
PDIA5	NM_001014125.1	Protein disulfide isomerase family A, member 5	1.274	1.274
IFI271I	NM_203410.1	Interferon, alpha-inducible protein 27 like 1	-0.814	-1.316
PLDN_PREDICTED	XM_229231.3	PREDICTED: pallidin	2.080	0.786
CROT	NM_031987.1	Carnitine O-octanoyltransferase	1.198	1.080
LOC500506	XM_575868.1	PREDICTED: similar to glyceraldehyde-3-phosphate dehydrogenase	0.942	1.164
Cyp3a23/3a1	NM_013105.1	Cytochrome P450, family 3, subfamily a, polypeptide 23/polypeptide 1	1.224	1.482
LOC499912	XM_575256.1	PREDICTED: similar to Ab2-305	0.742	1.087
CLDN1	NM_031699	Claudin 1	0.650	1.109
LOC498105	XM_573309.1	PREDICTED: similar to LRRGT00176	-0.767	-1.605
Akr1c13	NM_001014240	Aldo-keto reductase family 1, member C13	1.017	1.337
AKR1B7	NM_053781	Aldo-keto reductase family 1, member B7	-1.480	-2.019
LDHA	XM_001080828.1	Lactate dehydrogenase A	0.754	1.016

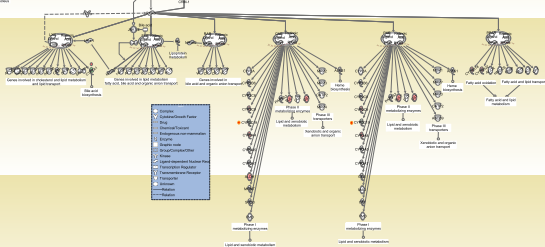
LPS(L)-1 Mediated Inhibition of ROR Function

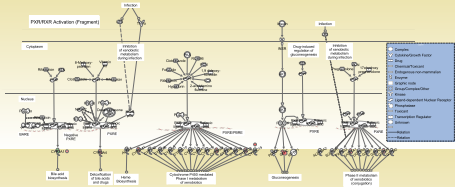
Cytoplasm

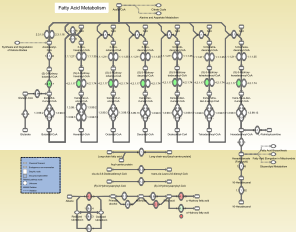
Hepatitis-mediated activation of LPS in bile



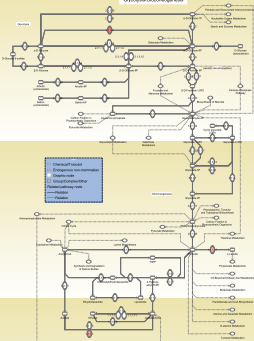
Nucleus





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Starch and Sucrose Metabolism

